SCORE Search Results Details for Application 10759514 and Search Result us-10-759-514-3.rng.

This page gives you Search Results detail for the Application 10759514 and Search Result us-10-759-514-3.rng.

start

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                          GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on:         May  7, 2006, 06:03:13 ; Search time 126.92 Seconds
                                          (without alignments)
                                          1260.261 Million cell updates/sec

Title:          US-10-759-514-3
Perfect score:  24
Sequence:       1 ccgggagagccatagtggtctgcg 24

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters:      9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        N_Geneseq_21:*
                 1:  geneseqn1980s:*
                 2:  geneseqn1990s:*
                 3:  geneseqn2000s:*
                 4:  geneseqn2001as:*
                 5:  geneseqn2001bs:*
                 6:  geneseqn2002as:*
                 7:  geneseqn2002bs:*
                 8:  geneseqn2003as:*
                 9:  geneseqn2003bs:*
                 10:  geneseqn2003cs:*
                 11:  geneseqn2003ds:*
                 12:  geneseqn2004as:*
                 13:  geneseqn2004bs:*
                 14:  geneseqn2005s:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES
                 %
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Result No.		Score	Query Match	Length	DB	ID	Description
1		24	100.0	24	10	ADD55637	Add55637 Oligonucl
2		24	100.0	24	10	ADD55641	Add55641 Oligonucl
3		24	100.0	24	14	ADV04767	Adv04767 Synthetic
4		24	100.0	24	14	ADV04754	Adv04754 Synthetic
5		24	100.0	24	14	ADZ75974	Adz75974 Hepatitis
6		24	100.0	24	14	ADZ75978	Adz75978 Hepatitis
7	c	24	100.0	27	2	AAQ64955	Aaq64955 Antisense
8	c	24	100.0	30	2	AAQ64950	Aaq64950 Antisense
9		24	100.0	37	2	AAX37631	Aax37631 HCV detec
10		24	100.0	50	3	AAA52575	Aaa52575 HCV RNA p
11	c	24	100.0	53	2	AAQ98103	Aaq98103 Label ext
12	c	24	100.0	70	2	AAT11268	Aat11268 Hepatitis
13	c	24	100.0	75	14	AEB94147	Aeb94147 Nucleic a
14		24	100.0	86	12	ADJ53747	Adj53747 HBV speci
15		24	100.0	102	4	AAC92379	Aac92379 HCV-RNA W
16		24	100.0	120	2	AAT69054	Aat69054 Hepatitis
17	c	24	100.0	120	14	AEB94144	Aeb94144 Nucleic a
18		24	100.0	120	14	AEB94143	Aeb94143 Nucleic a
19		24	100.0	131	14	ADW15169	Adw15169 HCV H77C
20		24	100.0	131	14	ADW15171	Adw15171 HCV from
21		24	100.0	131	14	ADW15170	Adw15170 HCV from
22		24	100.0	131	14	ADW15174	Adw15174 HCV from
23		24	100.0	131	14	ADW15172	Adw15172 HCV from
24		24	100.0	131	14	ADW15173	Adw15173 HCV from
25	c	24	100.0	140	2	AAT11269	Aat11269 Hepatitis
26	c	24	100.0	155	3	AAZ57775	Aaz57775 Hepatitis
27		24	100.0	159	2	AAQ43062	Aaq43062 -255 to -
28		24	100.0	159	2	AAQ43069	Aaq43069 -255 to -
29		24	100.0	159	2	AAQ43066	Aaq43066 -255 to -
30		24	100.0	159	2	AAQ43071	Aaq43071 -255 to -
31		24	100.0	177	2	AAQ79456	Aaq79456 HCV isola
32		24	100.0	177	2	AAQ68067	Aaq68067 HCV isola
33		24	100.0	177	2	AAQ79452	Aaq79452 HCV isola
34		24	100.0	177	2	AAQ79459	Aaq79459 HCV isola
35		24	100.0	177	2	AAQ79450	Aaq79450 HCV isola
36		24	100.0	177	2	AAQ79451	Aaq79451 HCV isola
37		24	100.0	177	2	AAQ68068	Aaq68068 HCV isola
38		24	100.0	177	2	AAQ79454	Aaq79454 HCV isola
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41		24	100.0	177	2	AAQ79457	Aaq79457 HCV isola
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43		24	100.0	177	2	AAQ79460	Aaq79460 HCV isola
44		24	100.0	177	2	AAQ79449	Aaq79449 HCV isola
45		24	100.0	177	2	AAQ79455	Aaq79455 HCV isola

ALIGNMENTS

RESULT 1
ADD55637
ID ADD55637 standard; DNA; 24 BP.
XX
AC ADD55637;
XX
DT 15-JAN-2004 (first entry)
XX
DE Oligonucleotide probe, PR2 #1, used to detect a HCV nucleic acid.
XX
KW HCV; fluorescent dye; fluorescent molecular beacon pair; lambda phage;

KW lambda phage-HCV hybrid amplicon; detection; diagnosis; HCV infection;
KW hepatitis; cirrhosis; antiviral therapy; probe; ss.
XX
OS Hepatitis C virus.
XX
PN US2003104582-A1.
XX
PD 05-JUN-2003.
XX
PF 04-DEC-2001; 2001US-00011855.
XX
PR 04-DEC-2001; 2001US-00011855.
XX
PA (BAUM/) BAUMANN R.
PA (HAMD/) HAMDAN H.
PA (LEWI/) LEWINSKI M.
XX
PI Baumann R, Hamdan H, Lewinski M;
XX
DR WPI; 2003-801237/75.
XX
PT Detecting hepatitis C virus (HCV) nucleic acid in a sample comprises
PT reverse transcribing and amplifying HCV nucleic acids with primer pair,
PT hybridizing amplicons with a labeled probe, and detecting a signal.
XX
PS Claim 1; Page 10; 11pp; English.
XX
CC The invention discloses a method for detecting the presence or amount of
CC Hepatitis C virus (HCV) nucleic acids in a sample comprising reverse
CC transcribing and amplifying any HCV nucleic acid present, reacting the
CC amplified nucleic acids with a probe in the presence of an enzyme that
CC cleaves the probe if specifically hybridised to HCV nucleic acids, and
CC detecting a signal from the probe. The detectable label is a fluorescent
CC dye or a fluorescent molecular beacon pair. Lambda phage HCV nucleic acid
CC hybrids are introduced into the test sample, reverse transcribed and
CC amplified using the pair of oligonucleotide primers to produce lambda
CC phage-HCV hybrid amplicons. The hybrids are hybridised to a control
CC oligonucleotide sequence (ADD55640) which is conjugated to 6-
CC carboxyfluorescein (FAM) and 6-carboxytetramethylrhodamine (TAMRA). The
CC test sample is chosen from serum, blood, plasma, cerebral spinal fluid,
CC synovial fluid, and urine. The nucleic acids are purified from the sample
CC prior to the reverse transcription and amplification step. The lambda
CC phage-HCV ribonucleic acid hybrids may be introduced into the test sample
CC prior to isolating nucleic acids from the sample. The method is useful
CC for detecting the presence or amount of hepatitis C virus (HCV) nucleic
CC acids in a test sample, for diagnosing HCV infection, which can lead to
CC chronic hepatitis and cirrhosis, for identification of individuals with
CC high viral replication, for monitoring patients on therapy and for
CC predicting whether antiviral therapy will be successful. The method is
CC specific and sensitive and exhibits a broad dynamic range of detection of
CC HCV nucleic acids and provides quantitative as well as qualitative
CC results. The sequence presented is an oligonucleotide probe used to
CC detect HCV nucleic acid.
XX
SQ Sequence 24 BP; 4 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24
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Db 1 CCGGGAGAGCCATAGTGGTCTGCG 24

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RESULT 2
ADD55641
ID   ADD55641 standard; DNA; 24 BP.
XX
AC   ADD55641;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Oligonucleotide probe, PR2 #2, used to detect a HCV nucleic acid.
XX
KW   HCV; fluorescent dye; fluorescent molecular beacon pair; lambda phage;
KW   lambda phage-HCV hybrid amplicon; detection; diagnosis; HCV infection;
KW   hepatitis; cirrhosis; antiviral therapy; probe; ss.
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= conjugated to 2'-chloro-7'-phenyl-1,4-
FT                    dichloro-6-carboxyfluorescein (VIC)"
FT   modified_base    24
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= conjugated to 6-
FT                    carboxytetramethylrhodamine (TAMRA)"
XX
PN   US2003104582-A1.
XX
PD   05-JUN-2003.
XX
PF   04-DEC-2001; 2001US-00011855.
XX
PR   04-DEC-2001; 2001US-00011855.
XX
PA   (BAUM/) BAUMANN R.
PA   (HAMD/) HAMDAN H.
PA   (LEWI/) LEWINSKI M.
XX
PI   Baumann R,  Hamdan H,  Lewinski M;
XX
DR   WPI; 2003-801237/75.
XX
PT   Detecting hepatitis C virus (HCV) nucleic acid in a sample comprises
PT   reverse transcribing and amplifying HCV nucleic acids with primer pair,
PT   hybridizing amplicons with a labeled probe, and detecting a signal.
XX
PS   Claim 5; Page 10; 11pp; English.
XX
CC   The invention discloses a method for detecting the presence or amount of
CC   Hepatitis C virus (HCV) nucleic acids in a sample comprising reverse
CC   transcribing and amplifying any HCV nucleic acid present, reacting the
CC   amplified nucleic acids with a probe in the presence of an enzyme that
CC   cleaves the probe if specifically hybridised to HCV nucleic acids, and
CC   detecting a signal from the probe. The detectable label is a fluorescent
CC   dye or a fluorescent molecular beacon pair. Lambda phage HCV nucleic acid
CC   hybrids are introduced into the test sample, reverse transcribed and
CC   amplified using the pair of oligonucleotide primers to produce lambda
CC   phage-HCV hybrid amplicons. The hybrids are hybridised to a control
CC   oligonucleotide sequence (ADD55640) which is conjugated to 6-
CC   carboxyfluorescein (FAM) and 6-carboxytetramethylrhodamine (TAMRA). The
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CC test sample is chosen from serum, blood, plasma, cerebral spinal fluid,
CC synovial fluid, and urine. The nucleic acids are purified from the sample
CC prior to the reverse transcription and amplification step. The lambda
CC phage-HCV ribonucleic acid hybrids may be introduced into the test sample
CC prior to isolating nucleic acids from the sample. The method is useful
CC for detecting the presence or amount of hepatitis C virus (HCV) nucleic
CC acids in a test sample, for diagnosing HCV infection, which can lead to
CC chronic hepatitis and cirrhosis, for identification of individuals with
CC high viral replication, for monitoring patients on therapy and for
CC predicting whether antiviral therapy will be successful. The method is
CC specific and sensitive and exhibits a broad dynamic range of detection of
CC HCV nucleic acids and provides quantitative as well as qualitative
CC results. The sequence presented is a labelled oligonucleotide probe used
CC to detect HCV nucleic acid.
XX
SQ Sequence 24 BP; 4 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24
||||||||||||||||||||||||
Db 1 CCGGGAGAGCCATAGTGGTCTGCG 24

RESULT 3
ADV04767
ID ADV04767 standard; DNA; 24 BP.
XX
AC ADV04767;
XX
DT 24-FEB-2005 (first entry)
XX
DE Synthetic PCR primer #18.
XX
KW Virucide; hepatitis C virus infection; ss; replicon; PCR; primer.
XX
OS Synthetic.
XX
PN WO2004104198-A1.
XX
PD 02-DEC-2004.
XX
PF 25-NOV-2003; 2003WO-JP015038.
XX
PR 26-MAY-2003; 2003JP-00148242.
PR 19-SEP-2003; 2003JP-00329115.
XX
PA (TORA) TORAY IND INC.
PA (TOKM-) TOKYO METROPOLITAN ORG MEDICAL RES.
PA (UYMA-) UNIV MAINZ GUTENBERG JOHANNES.
XX
PI Wakita T, Kato T, Date T;
XX
DR WPI; 2005-013292/01.
XX
PT Novel replicon RNA, having sequence of 5' and 3' untranslated region and
PT base sequence encoding NS3, NS4A, NS4B, NS5A and NS5B proteins on genomic
PT RNA of hepatitis C virus of genotype 2a, useful for treating hepatitis C
PT virus infection.
XX
PS Example 7; SEQ ID NO 33; 197pp; Japanese.
XX

CC The invention relates to replicon RNA from genotype 2a of hepatitis C
CC virus comprising a 5' untranslated region, a base sequence encoding NS3
CC protein, NS4A protein, NS4B protein, NS5A protein and NS5B protein, and a
CC 3' untranslated region. The invention also relates to a cell capable of
CC reproducing the replicon involving transducing the replicon RNA to a
CC cell, a method of producing a hepatitis C virus protein, a method of
CC screening a substance that promotes or suppresses the reproduction of
CC hepatitis C virus, involving culturing the replicon reproducing cell in
CC the presence of a test substance, and detecting the reproduction of
CC replicon RNA in the culture. Virucide. The replicon RNA is useful for
CC producing a replicon reproduction cell and for increasing the
CC reproduction efficiency of replicon RNA of hepatitis C virus of genotype
CC 2a. The cell and the replicon RNA are useful for producing a therapeutic
CC agent or a diagnostic agent for hepatitis C virus infection, for
CC producing a vaccine against hepatitis C virus infection and for screening
CC a substance that promotes or suppresses the reproduction of hepatitis C
CC virus. This sequence represents a PCR primer used in the scope of the
CC invention.
XX
SQ Sequence 24 BP; 4 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24
||||||||||||||||||||||||
Db 1 CCGGGAGAGCCATAGTGGTCTGCG 24

RESULT 4
ADV04754
ID ADV04754 standard; DNA; 24 BP.
XX
AC ADV04754;
XX
DT 24-FEB-2005 (first entry)
XX
DE Synthetic PCR primer #5.
XX
KW Virucide; hepatitis C virus infection; ss; replicon; PCR; primer.
XX
OS Synthetic.
XX
PN WO2004104198-A1.
XX
PD 02-DEC-2004.
XX
PF 25-NOV-2003; 2003WO-JP015038.
XX
PR 26-MAY-2003; 2003JP-00148242.
PR 19-SEP-2003; 2003JP-00329115.
XX
PA (TORA) TORAY IND INC.
PA (TOKM-) TOKYO METROPOLITAN ORG MEDICAL RES.
PA (UYMA-) UNIV MAINZ GUTENBERG JOHANNES.
XX
PI Wakita T, Kato T, Date T;
XX
DR WPI; 2005-013292/01.
XX
PT Novel replicon RNA, having sequence of 5' and 3' untranslated region and
PT base sequence encoding NS3, NS4A, NS4B, NS5A and NS5B proteins on genomic
PT RNA of hepatitis C virus of genotype 2a, useful for treating hepatitis C

PT virus infection.
XX
PS Example 5; SEQ ID NO 20; 197pp; Japanese.
XX
CC The invention relates to replicon RNA from genotype 2a of hepatitis C
CC virus comprising a 5' untranslated region, a base sequence encoding NS3
CC protein, NS4A protein, NS4B protein, NS5A protein and NS5B protein, and a
CC 3' untranslated region. The invention also relates to a cell capable of
CC reproducing the replicon involving transducing the replicon RNA to a
CC cell, a method of producing a hepatitis C virus protein, a method of
CC screening a substance that promotes or suppresses the reproduction of
CC hepatitis C virus, involving culturing the replicon reproducing cell in
CC the presence of a test substance, and detecting the reproduction of
CC replicon RNA in the culture. Virucide. The replicon RNA is useful for
CC producing a replicon reproduction cell and for increasing the
CC reproduction efficiency of replicon RNA of hepatitis C virus of genotype
CC 2a. The cell and the replicon RNA are useful for producing a therapeutic
CC agent or a diagnostic agent for hepatitis C virus infection, for
CC producing a vaccine against hepatitis C virus infection and for screening
CC a substance that promotes or suppresses the reproduction of hepatitis C
CC virus. This sequence represents a PCR primer used in the scope of the
CC invention.
XX
SQ Sequence 24 BP; 4 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24
||||||||||||||||||||||||
Db 1 CCGGGAGAGCCATAGTGGTCTGCG 24

RESULT 5
ADZ75974
ID ADZ75974 standard; DNA; 24 BP.
XX
AC ADZ75974;
XX
DT 14-JUL-2005 (first entry)
XX
DE Hepatitis C virus specific probe SEQ ID NO:3.
XX
KW DNA detection; RNA detection; hepatitis C virus infection;
KW antiinflammatory; hepatotropic; virucide; probe; ss.
XX
OS Hepatitis C virus.
OS Synthetic.
XX
PN US2005100889-A1.
XX
PD 12-MAY-2005.
XX
PF 13-OCT-2004; 2004US-00964302.
XX
PR 04-DEC-2001; 2001US-00011855.
XX
PA (QUES-) QUEST DIAGNOSTICS INVESTMENTS INC.
XX
PI Baumann R, Hamdan H, Lewinski M;
XX
DR WPI; 2005-345387/35.
XX

PT Detecting Hepatitis C virus (HCV) nucleic acids in a test sample, for
PT diagnosing HCV infection, comprises using oligonucleotide primers and
PT probes to amplify HCV and/or control nucleic acid sequences present in
PT the sample.
XX
PS Claim 1; SEQ ID NO 3; 13pp; English.
XX
CC The invention relates to a method for detecting the presence or amount of
CC Hepatitis C virus (HCV) nucleic acids in a test sample. The method
CC comprises: (a) introducing lambda phage-HCV nucleic acid hybrids into the
CC test sample; (b) reverse transcribing and amplifying: (i) HCV nucleic
CC acid if present in the sample and using a pair of oligonucleotide primers
CC having the sequences set forth in ADZ75972 and ADZ75973, to generate HCV
CC amplicons; and (ii) lambda phage-HCV hybrid nucleic acid using a pair of
CC oligonucleotide primers having the sequences set forth in ADZ75972 and
CC ADZ75973, to generate a lambda phage-HCV hybrid amplicons; (c)
CC hybridizing the HCV amplicons with an oligonucleotide probe comprising
CC the 24 bp sequence of ADZ75974 in the presence of an enzyme that cleaves
CC the probe when the probe hybridizes to the HCV nucleic acids, where the
CC probe is conjugated to a first detectable label that generates a
CC detectable signal upon the cleavage; (d) hybridizing the lambda phage-HCV
CC hybrid amplicons to a control oligonucleotide probe in the presence of an
CC enzyme that cleaves the control oligonucleotide probe when the control
CC probe hybridizes to the lambda phage-HCV hybrid amplicons, where the
CC control probe is conjugated to a second detectable label that generates a
CC detectable signal upon the cleavage; and (e) detecting a signal from the
CC first and second detectable labels, where the signal from the first
CC detectable label indicates the presence or amount of HCV nucleic acids in
CC the test sample. Also described is a composition of one or more
CC substantially purified oligonucleotides comprising the nucleotide
CC sequences mentioned in the specification, and a kit comprising materials
CC for performing the new method. The method and composition are useful for
CC diagnosing HCV infection or for qualitatively and quantitatively
CC detecting hepatitis C viral nucleic acids in a test sample. The present
CC sequence represents an HCV specific probe which is used in an example
CC from the present invention.
XX
SQ Sequence 24 BP; 4 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24
||||||||||||||||||||||||
Db 1 CCGGGAGAGCCATAGTGGTCTGCG 24

RESULT 6
ADZ75978
ID ADZ75978 standard; DNA; 24 BP.
XX
AC ADZ75978;
XX
DT 14-JUL-2005 (first entry)
XX
DE Hepatitis C virus specific probe SEQ ID NO:7.
XX
KW DNA detection; RNA detection; hepatitis C virus infection;
KW antiinflammatory; hepatotropic; virucide; probe; ss.
XX
OS Hepatitis C virus.
OS Synthetic.
XX

FH Key Location/Qualifiers
FT misc_binding 1
FT /*tag= a
FT /bound_moiety= "2'-chloro-7'-phenyl-1-4-dichloro-6-
FT carboxyfluorescein (VIC)"
FT misc_binding 24
FT /*tag= b
FT /bound_moiety= "6-carboxytetramethylrhodamine (TAMRA)"
XX
PN US2005100889-A1.
XX
PD 12-MAY-2005.
XX
PF 13-OCT-2004; 2004US-00964302.
XX
PR 04-DEC-2001; 2001US-00011855.
XX
PA (QUES-) QUEST DIAGNOSTICS INVESTMENTS INC.
XX
PI Baumann R, Hamdan H, Lewinski M;
XX
DR WPI; 2005-345387/35.
XX
PT Detecting Hepatitis C virus (HCV) nucleic acids in a test sample, for
PT diagnosing HCV infection, comprises using oligonucleotide primers and
PT probes to amplify HCV and/or control nucleic acid sequences present in
PT the sample.
XX
PS Example 2; SEQ ID NO 7; 13pp; English.
XX
CC The invention relates to a method for detecting the presence or amount of
CC Hepatitis C virus (HCV) nucleic acids in a test sample. The method
CC comprises: (a) introducing lambda phage-HCV nucleic acid hybrids into the
CC test sample; (b) reverse transcribing and amplifying: (i) HCV nucleic
CC acid if present in the sample and using a pair of oligonucleotide primers
CC having the sequences set forth in ADZ75972 and ADZ75973, to generate HCV
CC amplicons; and (ii) lambda phage-HCV hybrid nucleic acid using a pair of
CC oligonucleotide primers having the sequences set forth in ADZ75972 and
CC ADZ75973, to generate a lambda phage-HCV hybrid amplicons; (c)
CC hybridizing the HCV amplicons with an oligonucleotide probe comprising
CC the 24 bp sequence of ADZ75974 in the presence of an enzyme that cleaves
CC the probe when the probe hybridizes to the HCV nucleic acids, where the
CC probe is conjugated to a first detectable label that generates a
CC detectable signal upon the cleavage; (d) hybridizing the lambda phage-HCV
CC hybrid amplicons to a control oligonucleotide probe in the presence of an
CC enzyme that cleaves the control oligonucleotide probe when the control
CC probe hybridizes to the lambda phage-HCV hybrid amplicons, where the
CC control probe is conjugated to a second detectable label that generates a
CC detectable signal upon the cleavage; and (e) detecting a signal from the
CC first and second detectable labels, where the signal from the first
CC detectable label indicates the presence or amount of HCV nucleic acids in
CC the test sample. Also described is a composition of one or more
CC substantially purified oligonucleotides comprising the nucleotide
CC sequences mentioned in the specification, and a kit comprising materials
CC for performing the new method. The method and composition are useful for
CC diagnosing HCV infection or for qualitatively and quantitatively
CC detecting hepatitis C viral nucleic acids in a test sample. The present
CC sequence represents an HCV specific probe which is used in an example
CC from the present invention.
XX
SQ Sequence 24 BP; 4 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.059;

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Qy          1 CCGGGAGAGCCATAGTGGTCTGCG 24
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Db          1 CCGGGAGAGCCATAGTGGTCTGCG 24


RESULT 7
AAQ64955/c
ID   AAQ64955 standard; DNA; 27 BP.
XX
AC   AAQ64955;
XX
DT   19-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KW   inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-02104649.
XX
PR   25-AUG-1992;   92JP-00248796.
PR   03-MAR-1993;   93JP-00042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Seki M,  Honda Y,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT   genome - are useful as antiviral agents.
XX
PS   Claim 5; Page 82; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound i.e.
CC   it has a base sequence of 15-30 bases which is included within the 31
CC   bases from C at position 150 to G at position 180 of AAQ64913 and which
CC   contains at least 6 bases from C at position 175 to G at position 180.
CC   The antisense oligonucleotide is useful for inhibiting translation of HCV
CC   genes
XX
SQ   Sequence 27 BP; 5 A; 11 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 24;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.06;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGGGAGAGCCATAGTGGTCTGCG 24
              ||||||||||||||||||||||||
Db         25 CCGGGAGAGCCATAGTGGTCTGCG 2


RESULT 8
AAQ64950/c
ID   AAQ64950 standard; DNA; 30 BP.
XX
```

AC AAQ64950;
XX
DT 19-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KW inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-02104649.
XX
PR 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
PA (SEKI/) SEKI M.
XX
PI Seki M, Honda Y, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
PS Claim 5; Page 80; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 31
CC bases from C at position 150 to G at position 180 of AAQ64913 and which
CC contains at least 6 bases from C at position 151 to C at position 156.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
SQ Sequence 30 BP; 5 A; 11 C; 10 G; 4 T; 0 U; 0 Other;

  Query Match   100.0%; Score 24; DB 2; Length 30;
  Best Local Similarity 100.0%; Pred. No. 0.061;
  Matches   24; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCGGGAGAGCCATAGTGGTCTGCG 24
              ||||||||||||||||||||||||
Db   25 CCGGGAGAGCCATAGTGGTCTGCG 2

RESULT 9
AAX37631
ID AAX37631 standard; DNA; 37 BP.
XX
AC AAX37631;
XX
DT 08-JUL-1999 (first entry)
XX
DE HCV detecting primer #1.
XX
KW Detection; HCV; real time; PCR; reporter; fluorescent; primer; quencher;
KW fluorescence resonance energy transfer; ss.
XX
OS Synthetic.
OS Hepatitis C virus; Virus.

XX
PN JP11103899-A.
XX
PD 20-APR-1999.
XX
PF 30-SEP-1997; 97JP-00283042.
XX
PR 30-SEP-1997; 97JP-00283042.
XX
PA (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.
PA (SRLS-) SRL KK.
XX
DR WPI; 1999-305862/26.
XX
PT Measurement of HCV gene using real time detecting PCR and primer and
PT probe - is highly sensitive.
XX
PS Claim 1; Page 6; 8pp; Japanese.
XX
CC This invention describes a method for the measurement of an HCV gene by a
CC real time detecting PCR. The invention also describes a method where a
CC reporter fluorescent colour and a quencher fluorescent colour are
CC combined to an oligonucleotide and the fluorescence of the reporter
CC fluorescent colour is controlled by fluorescence resonance energy
CC transfer. The method can measure HCV exactly with high sensitivity
XX
SQ Sequence 37 BP; 6 A; 15 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGGGAGAGCCATAGTGGTCTGCG 24
              ||||||||||||||||||||||||
Db         10 CCGGGAGAGCCATAGTGGTCTGCG 33
```

RESULT 10
AAA52575
ID AAA52575 standard; DNA; 50 BP.
XX
AC AAA52575;
XX
DT 27-SEP-2000 (first entry)
XX
DE HCV RNA promoter primer, SEQ ID NO:13.
XX
KW Oligonucleotide; HCV genomic RNA; detection; amplification;
KW reverse transcription inhibition; translation inhibition; antiviral;
KW gene therapy; sense; promoter primer; reverse transcription-PCR;
KW RT-PCR primer; ss.
XX
OS Hepatitis C virus.
XX
PN EP1002878-A2.
XX
PD 24-MAY-2000.
XX
PF 18-NOV-1999; 99EP-00122092.
XX
PR 19-NOV-1998; 98JP-00329874.
XX
PA (TOYJ) TOSOH CORP.
XX

PI Toshiki T, Takahiko I, Juichi S;
XX
DR WPI; 2000-352431/31.
XX
PT Hepatitis C virus RNA-binding single-stranded oligo DNAs useful as
PT reagents for gene diagnosis involving cleavage, amplification and
PT detection of RNA and as an inhibitory drugs.
XX
PS Example 5; Page 15; 21pp; English.
XX
CC The invention relates to single-stranded antisense oligodeoxynucleotides
CC (AAA52563-A52568) which bind to various sites on the hepatitis C virus
CC (HCV) RNA genome, and to sense oligodeoxynucleotides (AAA52569-A52571)
CC corresponding to sites on the HCV genome. The oligonucleotides are useful
CC as primers in RT-PCR (reverse transcription-PCR) and the sense
CC oligonucleotides may also be used as promoter primers. The antisense
CC oligonucleotides may be used to inhibit translation or reverse
CC transcription of HCV RNA and may be used as probes for detection of HCV
CC RNA. Additionally, the antisense oligos may be linked to an RNA-cleaving
CC moiety to target single-stranded RNA cleavage or RNA heteroduplex
CC cleavage. The invention also encompasses methods of identifying and
CC preparing single-stranded oligodeoxynucleotides which bind to target
CC RNAs. The single-stranded oligodeoxynucleotides are useful as reagents
CC for genetic diagnosis involving cleavage, amplification and detection of
CC HCV RNA (as primers and probes), and as inhibitors of reverse
CC transcription or translation of HCV RNA. Sequences AAA42573-A52576
CC represent HCV RNA promoter primers used in an exemplification of the
CC invention
XX
SQ Sequence 50 BP; 15 A; 9 C; 15 G; 11 T; 0 U; 0 Other;

  Query Match   100.0%; Score 24; DB 3; Length 50;
  Best Local Similarity   100.0%; Pred. No. 0.066;
  Matches   24; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCGGGAGAGCCATAGTGGTCTGCG 24
              ||||||||||||||||||||||||
Db   26 CCGGGAGAGCCATAGTGGTCTGCG 49

RESULT 11
AAQ98103/c
ID AAQ98103 standard; DNA; 53 BP.
XX
AC AAQ98103;
XX
DT 05-FEB-1996 (first entry)
XX
DE Label extender probe used in an improved sandwich hybridisation assay.
XX
KW Probe; nucleotide; solution phase sandwich hybridisation assay;
KW competitive; analyte binding sequence; background signal reduction; ss.
XX
OS Synthetic.
XX
PN WO9516055-A1.
XX
PD 15-JUN-1995.
XX
PF 07-DEC-1994; 94WO-US014119.
XX
PR 08-DEC-1993; 93US-00164388.
XX
PA (CHIR) CHIRON CORP.

XX
PI Urdea MS, Fultz T, Warner BD, Collins M;
XX
DR WPI; 1995-224335/29.
XX
PT Soln. phase sandwich hybridisation assays for nucleic acid(s) - with
PT capture extender molecules or competitive oligo:nucleotide(s) to minimise
PT background signal, increasing sensitivity and selectivity.
XX
PS Example 1; Page 33; 86pp; English.
XX
CC AAQ98100-Q98105 are label extender probes (LEs) used in a variation of a
CC new improved method of a solution phase sandwich hybridisation assay in
CC which LEs are used with a capture probe (CP). One label extender probe
CC binds the target DNA and another binds to a labelled probe (LP). The new
CC method minimises background signals (caused by non-specific
CC hybridisation), this improves both sensitivity and selectivity of the
CC assay without increasing cost or time
XX
SQ Sequence 53 BP; 9 A; 15 C; 20 G; 9 T; 0 U; 0 Other;

  Query Match   100.0%; Score 24; DB 2; Length 53;
  Best Local Similarity   100.0%; Pred. No. 0.066;
  Matches   24; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCGGGAGAGCCATAGTGGTCTGCG 24
              ||||||||||||||||||||||||
Db   44 CCGGGAGAGCCATAGTGGTCTGCG 21

RESULT 12
AAT11268/c
ID AAT11268 standard; RNA; 70 BP.
XX
AC AAT11268;
XX
DT 26-JUN-1996 (first entry)
XX
DE Hepatitis C virus partial 5'-UTR antisense RNA AS3.
XX
KW Antisense; therapy; complementary; HCV; 5'-untranslated region;
KW hepatitis C virus; inhibition; infection; treatment; stem-loop;
KW clone 2-1; ss.
XX
OS Hepatitis C virus.
XX
PN JP07303485-A.
XX
PD 21-NOV-1995.
XX
PF 13-MAY-1994;   94JP-00124609.
XX
PR 13-MAY-1994;   94JP-00124609.
XX
PA (TOFU) TONEN CORP.
XX
DR WPI; 1996-035187/04.
XX
PT Hepatitis C virus (HCV) anti:sense RNA - inhibits HCV structural gene
PT expression in vivo for treatment of HCV infection.
XX
PS Claim 2; Page 9; 12pp; Japanese.
XX
CC The present sequence is a specifically claimed example of RNA that is

```
CC   complementary (i.e. antisense) to part of the 5'-untranslated region of
CC   the hepatitis C virus genome sequence contained in clone 2-1. The 5'-UTR
CC   includes several stem-loop sequences.The antisense RNA is useful for
CC   inhibiting expression of HCV structural genes and thereby inhibiting
CC   viral replication in vivo. The antisense therapy can be used in addition
CC   to conventional interferon treatment of HCV infections
XX
SQ   Sequence 70 BP; 10 A; 21 C; 25 G; 0 T; 14 U; 0 Other;

  Query Match             100.0%;  Score 24;  DB 2;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 0.069;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGGGAGAGCCATAGTGGTCTGCG 24
              ||||||||||||||||||||||||
Db         51 CCGGGAGAGCCATAGTGGTCTGCG 28


RESULT 13
AEB94147/c
ID   AEB94147 standard; DNA; 75 BP.
XX
AC   AEB94147;
XX
DT   06-OCT-2005  (first entry)
XX
DE   Nucleic acid detection method target sequence LTar-HCV.
XX
KW   ss; probe; microorganism detection; DNA detection; RNA detection.
XX
OS   Hepatitis C virus.
XX
PN   WO2005071401-A2.
XX
PD   04-AUG-2005.
XX
PF   14-JAN-2005; 2005WO-US001378.
XX
PR   15-JAN-2004; 2004US-0536978P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Shyamala V,  Nguyen SH;
XX
DR   WPI; 2005-564246/57.
XX
PT   Detecting a nucleic acid target sequence comprises contacting the sample
PT   with a capture probe conjugate, a reporter probe and a detectable
PT   reporter moiety.
XX
PS   Example 1; SEQ ID NO 22; 42pp; English.
XX
CC   The invention relates to a method of detecting a nucleic acid target
CC   sequence in a sample comprising contacting the sample with a capture
CC   probe conjugate, a reporter probe and a detectable reporter moiety. The
CC   method comprises: (i) contacting the sample with a capture probe
CC   conjugate, a reporter probe and a detectable reporter moiety, under
CC   conditions allowing formation of a complex including the nucleic acid
CC   target sequence, if present, the capture probe conjugate, the reporter
CC   probe and the detectable reporter moiety, where the capture probe
CC   conjugate and the reporter probe each comprise an oligonucleotide that is
CC   capable of specifically hybridizing to the nucleic acid target sequence
CC   and where the capture probe conjugate and the reporter probe do not
CC   hybridize to the same or overlapping regions of the nucleic acid target
```

CC sequence. The capture probe conjugate comprises a substrate having a
CC distinguishable spectral signal signature that uniquely identifies the
CC capture probe conjugate, where the reporter probe comprises one member of
CC a binding pair and the detectable reporter moiety comprises the other
CC member of the binding pair, and where the detectable reporter moiety
CC comprises a detectable label; and (ii) detecting a signal from the
CC capture probe conjugate substrate and the detectable reporter moiety
CC label individually from each complex so formed. Also included is a kit
CC for a multiplex assay for detecting the presence of nucleic acid target
CC sequences in a sample, comprising: capture probe conjugates, reporter
CC probes and a detectable reporter moiety, where each member of the capture
CC probe conjugates is specific for one member of the target sequences (the
CC specific capture probe conjugate) and each member of the reporter probes
CC is specific for one member of the target sequences (the specific reporter
CC probe). The nucleic acid target sequence is a sequence from a pathogen
CC nucleic acid, where the pathogen is a virus selected from HIV, HBV, HCV,
CC HAV, parvovirus B19, West Nile Virus, hantavirus or SARS. The method and
CC kit are useful for detecting a nucleic acid target sequence in a sample.
CC The present sequence represents a nucleic acid detection method target
CC sequence.
XX
SQ Sequence 75 BP; 14 A; 24 C; 23 G; 14 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 75;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24
||||||||||||||||||||||||
Db 27 CCGGGAGAGCCATAGTGGTCTGCG 4

RESULT 14
ADJ53747
ID ADJ53747 standard; DNA; 86 BP.
XX
AC ADJ53747;
XX
DT 06-MAY-2004 (first entry)
XX
DE HBV specific molecular beacon target #16.
XX
KW ss; capture oligonucleotide; HBV; HIV-1; HCV; donated blood screening.
XX
OS Hepatitis B virus.
XX
PN WO2003106714-A1.
XX
PD 24-DEC-2003.
XX
PF 13-JUN-2003; 2003WO-US018993.
XX
PR 14-JUN-2002; 2002US-0389393P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Linnen JM, Kolk DP, Dockter JM, Getman DK, Yoshimura T;
PI Ho-Sing-Loy M, Stringfellow LA;
XX
DR WPI; 2004-082210/08.
XX
PT Capture oligonucleotide composition useful for detection of hepatitis B
PT virus (HBV), comprising polynucleotide having HBV-complementary sequence
PT which is immobilized on solid support.

XX
PS Example 10; SEQ ID NO 141; 112pp; English.
XX
CC The invention relates to a capture oligonucleotide composition comprising
CC an hepatitis B virus (HBV)-complementary sequence polynucleotide
CC immobilised to a solid support. The composition is useful for detecting
CC nucleic acids of HBV and/of HIV-1 and/or HCV in biological sample such as
CC blood, serum, plasma or other body fluid or tissue to be tested. The
CC composition can be used either in diagnostic application or for screening
CC donated blood and that products or other tissues that may contain
CC infectious particles. The composition facilitates detection of very low
CC levels of HBV nucleic acids. The composition allows selective detection
CC of nucleic acids of HBV and/or HIV and/or HCV. The present sequence is
CC used in the exemplification of the invention.
XX
SQ Sequence 86 BP; 17 A; 26 C; 27 G; 16 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 12; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGGGAGAGCCATAGTGGTCTGCG 24
              ||||||||||||||||||||||||
Db         38 CCGGGAGAGCCATAGTGGTCTGCG 61
```

RESULT 15
AAC92379
ID AAC92379 standard; RNA; 102 BP.
XX
AC AAC92379;
XX
DT 26-MAR-2001 (first entry)
XX
DE HCV-RNA WQ-RNA nucleotide sequence SEQ ID NO:7.
XX
KW Amplification; analysis; RNA transcription; RNA polymerase; detection;
KW bacterium; virus; foodstuff; soil; environmental water; seawater;
KW house dust; ss.
XX
OS Synthetic.
XX
PN WO200075371-A1.
XX
PD 14-DEC-2000.
XX
PF 05-JUN-2000; 2000WO-JP003647.
XX
PR 04-JUN-1999; 99JP-00157653.
XX
PA (TOYJ) TOSOH CORP.
XX
PI Ishizuka T, Ishiguro T, Saitoh J, Sakai T;
XX
DR WPI; 2001-061738/07.
XX
PT Potentiated method for amplification of nucleic acids for detection in
PT biological samples.
XX
PS Example 3; Page 38; 42pp; Japanese.
XX
CC The present invention describes a method for amplifying a specific RNA
CC from a sample. The method comprises generating from the template RNA in
CC the sample a two-stranded DNA, which contains sequences complementary to

CC and homologous with the RNA sequence, and a transcription promoter. RNA
CC is transcribed from the two-stranded DNA using an RNA polymerase, in as
CC reaction mixture comprising inosine triphosphate (ITP), Adenosine
CC triphosphate (ATP), uridine triphosphate (UTP), cytidine triphosphate
CC (CTP) and guanosine triphosphate (GTP), and the reaction cycle is
CC repeated as necessary. The method can be used for the detection and assay
CC of specific RNA sequences, such as those occurring in bacteria and
CC viruses, in samples such as foodstuffs, soil, environmental waters,
CC seawater and house dust. The addition of ITP increases the efficiency of
CC the amplification reaction. The present sequence represents an
CC oligonucleotide used in an example from the present invention, for the
CC exemplification of the method of the invention
XX
SQ Sequence 102 BP; 23 A; 29 C; 25 G; 0 T; 25 U; 0 Other;

Query Match 100.0%; Score 24; DB 4; Length 102;
Best Local Similarity 83.3%; Pred. No. 0.073;
Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGGGAGAGCCATAGTGGTCTGCG 24
              |||||||||||||:||:||:|:|||
Db         13 CCGGGAGAGCCAUAGUGGUCUGCG 36
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SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 10759 Result us-10-759-514-6.rge.

This page gives you Search Results detail for the Application 10759514 and Search Result us-10-759-514-start

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                          GenCore version 5.1.8
                    Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters:      11766282

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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                7:  gb_ph:*
                8:  gb_pr:*
                9:  gb_ro:*
                10:  gb_sts:*
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                13:  gb_vi:*
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                15:  gb_pl:*

      Pred. No. is the number of results predicted by chance to have a
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                                    SUMMARIES

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c	2	22	100.0	5557	6	CQ830721	CQ830721 Sequence
c	3	22	100.0	5557	6	CQ832100	CQ832100 Sequence
c	4	22	100.0	48502	7	LAMCG	J02459 Bacteriopha
c	5	19.4	88.2	44139	2	AY190942	AY190942 Drosophil
c	6	18.8	85.5	30844	15	AC158186	AC158186 Selaginel
	7	18.8	85.5	104771	9	AL603830	AL603830 Mouse DNA
	8	18.8	85.5	206431	14	AC161885	AC161885 Gallus ga
	9	18.8	85.5	244279	14	AC163712	AC163712 Gallus ga
	10	18.8	85.5	248883	14	AC098544	AC098544 Rattus no
	11	18.8	85.5	259215	14	AC118088	AC118088 Rattus no
	12	18.8	85.5	262976	14	AC120483	AC120483 Rattus no
c	13	18.8	85.5	264908	9	AC096627	AC096627 Mus muscu
	14	18.4	83.6	110000	1	BA000023_21	Continuation (22 o
	15	18.4	83.6	110000	1	BA000023_22	Continuation (23 o
	16	18.4	83.6	145993	8	AC098972	AC098972 Homo sapi
	17	18.4	83.6	167304	9	AL928678	AL928678 Mouse DNA
c	18	18.4	83.6	169111	14	CR954168	CR954168 Danio rer
	19	18.4	83.6	197839	9	AL845466	AL845466 Mouse DNA
	20	18.4	83.6	207127	14	AC069496	AC069496 Homo sapi
c	21	18.4	83.6	213005	8	AP005059	AP005059 Homo sapi
	22	18.4	83.6	220618	14	AC131892	AC131892 Atelerix
c	23	18.4	83.6	237739	14	AC134520	AC134520 Atelerix
	24	17.8	80.9	905	10	BV576244	BV576244 G591P6073
c	25	17.8	80.9	32931	15	AC158190	AC158190 Selaginel
	26	17.8	80.9	37165	15	AC158184	AC158184 Selaginel
	27	17.8	80.9	39857	8	AC002522	AC002522 Homo sapi
	28	17.8	80.9	44873	8	AC004461	AC004461 Homo sapi
	29	17.8	80.9	59030	5	BX324184	BX324184 Zebrafish
	30	17.8	80.9	97351	8	AC015853	AC015853 Homo sapi
	31	17.8	80.9	108400	8	HUMDGCRCEN	L77570 Homo sapien
c	32	17.8	80.9	110000	1	BA000019_08	Continuation (9 of
	33	17.8	80.9	110000	15	CR382131_32	Continuation (33 o
	34	17.8	80.9	114540	8	AC107426	AC107426 Homo sapi
	35	17.8	80.9	125630	14	AC090650	AC090650 Arabidops
c	36	17.8	80.9	149939	5	AL935281	AL935281 Zebrafish
c	37	17.8	80.9	153284	8	AC078925	AC078925 Homo sapi
c	38	17.8	80.9	157327	14	CR450752	CR450752 Danio rer
	39	17.8	80.9	157904	8	AC108486	AC108486 Homo sapi
	40	17.8	80.9	159868	8	AC122129	AC122129 Homo sapi
c	41	17.8	80.9	159876	8	HS253P07	AL354000 Homo from
c	42	17.8	80.9	159994	8	AC157498	AC157498 Pan trogl
c	43	17.8	80.9	160256	5	BX950187	BX950187 Zebrafish
	44	17.8	80.9	160583	14	AC154944	AC154944 Monodelph
	45	17.8	80.9	169665	14	AC144566	AC144566 Homo sapi

ALIGNMENTS

RESULT 1
AF059603/c
LOCUS AF059603 1337 bp mRNA linear VRL 30-JAN-2000
DEFINITION Wheat rosette stunt virus nucleocapsid protein (N) mRNA, partial cds.
ACCESSION AF059603
VERSION AF059603.1 GI:6815246
KEYWORDS .
SOURCE Wheat rosette stunt virus
ORGANISM Wheat rosette stunt virus
Viruses; ssRNA negative-strand viruses; Mononegavirales; Rhabdoviridae; unclassified Rhabdoviridae.

```
REFERENCE   1  (bases 1 to 1337)
  AUTHORS   Gong,Z.X.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-1998) Virology Laboratory, Shanghai Institute of
            Biochemistry, Chinese Academy of Science, 320 Yue Yang Rd.,
            Shanghai 200031, P.R. China
FEATURES             Location/Qualifiers
     source          1. .1337
                     /organism="Wheat rosette stunt virus"
                     /mol_type="mRNA"
                     /db_xref="taxon:75890"
     gene            <1. .1337
                     /gene="N"
     CDS             <1. .1209
                     /gene="N"
                     /codon_start=1
                     /product="nucleocapsid protein"
                     /protein_id="AAF28467.1"
                     /db_xref="GI:6815247"
                     /translation="TFTKGDAERWVSTTKKASDSAFWLEVEGNSMTAPNGSKPSLAVI
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                     KSRMMLAKSHRHPLDCLFVCQESYSSYTFCHRLLLRHVIIRNLLAYYRPIVFLIYKVD
                     DTVLRCTGDSMILRHIVIVHRIYIYIIICINRVACSATVAHRRYGRARRHVVCRNVVR
                     LAGELPIVRVLNDFQLLPILHIFCMREFVPPPTDHLSLYATVPRLLCAGATLQTSFSV
                     HATVANDLPRNWLASYYRFCKNSPPHIKSIRSLPISVVISIFIIFMIPRKNLPSLLAR
                     IQYSFPIIGKSFKSIIGFRFASINSDCSCRKRCGRTIFPYNFYERVSLSNHFTQVLPC
                     LQTIPVSNIK"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 13;  Length 1337;
  Best Local Similarity   100.0%;  Pred. No. 4.5;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TTGGCAACAGTGGCATGCACCG 22
              ||||||||||||||||||||||
Db        845 TTGGCAACAGTGGCATGCACCG 824


RESULT 2
CQ830721/c
LOCUS       CQ830721               5557 bp    DNA     linear   PAT 12-JUL-2004
DEFINITION  Sequence 24 from Patent WO2004055215.
ACCESSION   CQ830721
VERSION     CQ830721.1  GI:50251007
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Otte,A.P. and van Blokland,H.J.
  TITLE     A method for improving protein production
  JOURNAL   Patent: WO 2004055215-A 24 01-JUL-2004;
            Chromagenics B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .5557
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="lambda fragment 22425-27972"
ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 5557;
  Best Local Similarity   100.0%;  Pred. No. 4;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 TTGGCAACAGTGGCATGCACCG 22
              ||||||||||||||||||||||
Db       1968 TTGGCAACAGTGGCATGCACCG 1947


RESULT 3
CQ832100/c
LOCUS       CQ832100                5557 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 9 from Patent WO2004056986.
ACCESSION   CQ832100
VERSION     CQ832100.1  GI:50831814
KEYWORDS    .
SOURCE      Bacteriophage lambda
  ORGANISM  Bacteriophage lambda
            Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
            Lambda-like viruses.
REFERENCE   1
  AUTHORS   Otte,A.P., Kwaks,T.H. and Sewalt,R.G.
  TITLE     Means and methods for producing a protein through chromatin openers
            that are capable of rendering chromatin more accessible to
            transcription factors
  JOURNAL   Patent: WO 2004056986-A 9 08-JUL-2004;
            Chromagenics B.V. (NL)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             100.0%;  Score 22;  DB 6;  Length 5557;
  Best Local Similarity   100.0%;  Pred. No. 4;
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Qy          1 TTGGCAACAGTGGCATGCACCG 22
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RESULT 4
LAMCG/c
LOCUS       LAMCG                   48502 bp    DNA     circular PHG 17-APR-2002
DEFINITION  Bacteriophage lambda, complete genome.
ACCESSION   J02459 M17233 M24325 V00636 X00906
VERSION     J02459.1  GI:215104
KEYWORDS    DNA-binding protein; circular; coat protein; complete genome;
            origin of replication; repressor; unidentified reading frame.
SOURCE      Bacteriophage lambda
  ORGANISM  Bacteriophage lambda
            Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
            Lambda-like viruses.
REFERENCE   2  (bases 1 to 12)
  AUTHORS   Wu,R. and Taylor,E.
  TITLE     Nucleotide sequence analysis of DNA. II. Complete nucleotide
            sequence of the cohesive ends of bacteriophage lambda DNA
  JOURNAL   J. Mol. Biol. 57 (3), 491-511 (1971)
   PUBMED   4931680
REFERENCE   3  (bases 45493 to 45963)
  AUTHORS   Imada,M. and Tsugita,A.
  TITLE     Amino acid sequence of lambda phage endolysin
  JOURNAL   Nature New Biol. 233, 230-231 (1971)
REFERENCE   4  (sites)
  AUTHORS   Weigel,P.H., Englund,P.T., Murray,K. and Old,R.W.
```

TITLE The 3'-terminal nucleotide sequences of bacteriophage lambda DNA
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 70 (4), 1151-1155 (1973)
PUBMED 4515613

REFERENCE 5 (bases 38597 to 38672)
AUTHORS Dahlberg,J.E. and Blattner,F.R.
TITLE In vitro transcription products of lambda DNA: Nucleotide sequences and regulatory sites
JOURNAL (in) Fox,C.F. and Robinson,W.S. (Eds.); VIRUS RESEARCH. PROCEEDINGS OF 1973 ICN-UCLA SYMPOSIUM: 533-544; Academic Press, New York (1973)

REFERENCE 6 (bases 37945 to 38027)
AUTHORS Maniatis,T., Ptashne,M., Backman,K., Kield,D., Flashman,S., Jeffrey,A. and Maurer,R.
TITLE Recognition sequences of repressor and polymerase in the operators of bacteriophage lambda
JOURNAL Cell 5 (2), 109-113 (1975)
PUBMED 1095210

REFERENCE 7 (bases 35583 to 35600)
AUTHORS Kleid,D.G., Agarwal,K.L. and Khorana,H.G.
TITLE The nucleotide sequence in the promoter region of the gene N in bacteriophage lambda
JOURNAL J. Biol. Chem. 250 (14), 5574-5582 (1975)
PUBMED 167018

REFERENCE 8 (bases 35434 to 35618)
AUTHORS Dahlberg,J.E. and Blattner,F.R.
TITLE Sequence of the promoter-operator proximal region of the major leftward RNA of bacteriophage lambda
JOURNAL Nucleic Acids Res. 2 (9), 1441-1458 (1975)
PUBMED 1178525

REFERENCE 9 (bases 37945 to 38018)
AUTHORS Maniatis,T., Jeffrey,A. and Kleid,D.G.
TITLE Nucleotide sequence of the rightward operator of phage lambda
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 72 (3), 1184-1188 (1975)
PUBMED 1055375

REFERENCE 10 (bases 44588 to 44773)
AUTHORS Sklar,J., Yot,P. and Weissman,S.M.
TITLE Determination of genes, restriction sites, and DNA sequences surrounding the 6S RNA template of bacteriophage lambda
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 72 (5), 1817-1821 (1975)
PUBMED 1098044

REFERENCE 11 (bases 37905 to 37989)
AUTHORS Walz,,A., Pirrotta,V. and Ineichen,K.
TITLE Lambda repressor regulates the switch between PR and Prm promoters
JOURNAL Nature 262 (5570), 665-669 (1976)
PUBMED 958438

REFERENCE 12 (bases 37946 to 38039)
AUTHORS Smith,G.R., Eisen,H., Reichardt,L. and Hedgepeth,J.
TITLE Deletions of lambda phage locating a prm mutation within the rightward operator
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 73 (3), 712-716 (1976)
PUBMED 1062780

REFERENCE 13 (bases 35578 to 35667; 37903 to 38027)
AUTHORS Ptashne,M., Backman,K., Humayun,M.Z., Jeffrey,A., Maurer,R., Meyer,B. and Sauer,R.T.
TITLE Autoregulation and function of a repressor in bacteriophage lambda
JOURNAL Science 194 (4261), 156-161 (1976)
PUBMED 959843

REFERENCE 14 (bases 35578 to 35667)
AUTHORS Humayun,Z., Jeffrey,A. and Ptashne,M.
TITLE Completed DNA sequences and organization of repressor-binding sites in the operators of phage lambda
JOURNAL J. Mol. Biol. 112 (2), 265-277 (1977)
PUBMED 875019

REFERENCE 15 (bases 38610 to 38732)

AUTHORS Scherer,G., Hobom,G. and Kossel,H.
TITLE DNA base sequence of the po promoter region of phage lamdba
JOURNAL Nature 265 (5590), 117-121 (1977)
PUBMED 834253
REFERENCE 16 (bases 38041 to 38241)
AUTHORS Roberts,T.M., Shimatake,H., Brady,C. and Rosenberg,M.
TITLE Sequence of Cro gene of bacteriophage lambda
JOURNAL Nature 270 (5634), 274-275 (1977)
PUBMED 593347
REFERENCE 17 (bases 27616 to 28935)
AUTHORS Davies,R.W., Schreier,P.H. and Buchel,D.E.
TITLE Nucleotide sequence of the attachment site of coliphage lambda
JOURNAL Nature 270 (5639), 757-760 (1977)
PUBMED 593399
REFERENCE 18 (bases 37206 to 37263; 37914 to 37970)
AUTHORS Humayun,Z.
TITLE DNA sequence at the end of the cI gene in bacteriophage lambda
JOURNAL Nucleic Acids Res. 4 (7), 2137-2143 (1977)
PUBMED 909767
REFERENCE 19 (bases 27617 to 27934)
AUTHORS Landy,A. and Ross,W.
TITLE Viral integration and excision: structure of the lambda att sites
JOURNAL Science 197 (4309), 1147-1160 (1977)
PUBMED 331474
REFERENCE 20 (bases 39062 to 39170)
AUTHORS Denniston-Thompson,K., Moore,D.D., Kruger,K.E., Furth,M.E. and Blattner,F.R.
TITLE Physical structure of the replication origin of bacteriophage lambda
JOURNAL Science 198 (4321), 1051-1056 (1977)
PUBMED 929187
REFERENCE 21 (bases 44467 to 44807)
AUTHORS Sklar,J.L.
TITLE Structure and function of two regions of DNA controlling the synthesis of prokaryotic RNAs
JOURNAL Thesis (1977)
REFERENCE 22 (sites)
AUTHORS Adhya,S. and Gottesman,M.
TITLE Control of transcription termination
JOURNAL Annu. Rev. Biochem. 47, 967-996 (1978)
PUBMED 354508
REFERENCE 23 (bases 13 to 72; 48391 to 48502)
AUTHORS Nichols,B.P. and Donelson,J.E.
TITLE 178-Nucleotide sequence surrounding the cos site of bacteriophage lambda DNA
JOURNAL J. Virol. 26 (2), 429-434 (1978)
PUBMED 666898
REFERENCE 24 (bases 37938 to 38016; 35589 to 35666)
AUTHORS Flashman,S.M.
TITLE Mutational analysis of the operators of bacteriophage lambda
JOURNAL Mol. Gen. Genet. 166 (1), 61-73 (1978)
PUBMED 368570
REFERENCE 25 (bases 37990 to 38982)
AUTHORS Schwarz,E., Scherer,G., Hobom,G. and Kossel,H.
TITLE Nucleotide sequence of cro, cII and part of the O gene in phage lambda DNA
JOURNAL Nature 272 (5652), 410-414 (1978)
PUBMED 264238
REFERENCE 26 (bases 38212 to 38362)
AUTHORS Rosenberg,M., Court,D., Shimatake,H., Brady,C. and Wulff,D.L.
TITLE The relationship between function and DNA sequence in an intercistronic regulatory region in phage lambda
JOURNAL Nature 272 (5652), 414-423 (1978)
PUBMED 634366

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REFERENCE   27 (bases 37224 to 37940)
  AUTHORS   Sauer,R.T.
  TITLE     DNA sequence of the bacteriophage gama cI gene
  JOURNAL   Nature 276 (5685), 301-302 (1978)
   PUBMED   714163
REFERENCE   28 (bases 38597 to 39688)
  AUTHORS   Scherer,G.
  TITLE     Nucleotide sequence of the O gene and of the origin of replication
            in bacteriophage lambda DNA
  JOURNAL   Nucleic Acids Res. 5 (9), 3141-3156 (1978)
   PUBMED   704348
REFERENCE   29 (bases 29711 to 29811; 31043 to 31058)
  AUTHORS   Davies,R.W., Schreier,P.H. and Buchel,D.E.
  TITLE     Determination of the endpoints of partial deletion mutants of the
            attachment site of bacteriophage lambda by DNA sequencing
  JOURNAL   Nucleic Acids Res. 5 (9), 3209-3218 (1978)
   PUBMED   704352
REFERENCE   30 (bases 21661 to 31129)
  AUTHORS   Hoess,R.H. and Landy,A.
  TITLE     Structure of the lambda att sites generated by int-dependent
            deletions
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 75 (11), 5437-5441 (1978)
   PUBMED   364480
REFERENCE   31 (bases 38453 to 38500)
  AUTHORS   Sprague,K.U., Faulds,D.H. and Smith,G.R.
  TITLE     A single base-pair change creates a Chi recombinational hotspot in
            bacteriophage lambda
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 75 (12), 6182-6186 (1978)
   PUBMED   282634
REFERENCE   32 (bases 27711 to 27826)
  AUTHORS   Ross,W., Landy,A., Kikuchi,Y. and Nash,H.
  TITLE     Interaction of int protein with specific sites on lambda att DNA
  JOURNAL   Cell 18 (2), 297-307 (1979)
   PUBMED   159130
REFERENCE   33 (bases 38008 to 39328)
  AUTHORS   Moore,D.D., Denniston-Thompson,K., Kruger,K.E., Furth,M.E.,
            Williams,B.G., Daniels,D.L. and Blattner,F.R.
  TITLE     Dissection and comparative anatomy of the origins of replication of
            lambdoid phages
  JOURNAL   Cold Spring Harb. Symp. Quant. Biol. 43 Pt 1, 155-163 (1979)
   PUBMED   157834
REFERENCE   34 (bases 38470 to 39189)
  AUTHORS   Hobom,G., Grosschedl,R., Lusky,M., Scherer,G., Schwarz,E. and
            Kossel,H.
  TITLE     Functional analysis of the replicator structure of lambdoid
            bacteriophage DNAs
  JOURNAL   Cold Spring Harb. Symp. Quant. Biol. 43 Pt 1, 165-178 (1979)
   PUBMED   157835
REFERENCE   35 (bases 38453 to 38500)
  AUTHORS   Smith,G.R., Faulds,D.H. and Sprague,K.U.

  Query Match             100.0%;  Score 22;  DB 7;  Length 48502;
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RESULT 5
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DEFINITION  Drosophila pseudoobscura clone DPSF01_33_N22 (D1412) genomic
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ACCESSION   AY190942
VERSION     AY190942.1  GI:27374267
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  ORGANISM  Drosophila pseudoobscura
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            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 44139)
  AUTHORS   Bergman,C.M., Pfeiffer,B.D., Rincon-Limas,D.E., Hoskins,R.A.,
            Gnirke,A., Mungall,C.J., Wang,A.M., Kronmiller,B., Pacleb,J.,
            Park,S., Stapleton,M., Wan,K., George,R.A., de Jong,P.J., Botas,J.,
            Rubin,G.M. and Celniker,S.E.
  TITLE     Assessing the impact of comparative genomic sequence data on the
            functional annotation of the Drosophila genome
  JOURNAL   Genome Biol. 3 (12), research0086 (2002)
  REMARK    http://genomebiology.com/2002/3/12/research/0086
REFERENCE   2  (bases 1 to 44139)
  AUTHORS   Pfeiffer,B.D., Bergman,C.M., Gnirke,A., Hoskins,R.A., Moshrefi,A.,
            Mungall,C.J., Pacleb,J., Wang,A.M., Park,S., Wan,K., George,R.A.,
            Rubin,G.M. and Celniker,S.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-DEC-2002) Berkeley Drosophila Genome Project,
            Lawrence Berkeley National Laboratory, 1 Cyclotron Rd, Berkeley, CA
            94720, USA
COMMENT     Gene annotations are preliminary because they are based solely on
            alignments of conceptually translated gene models to the
            corresponding gene model in Drosophila melanogaster.  As a
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ORIGIN

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RESULT 6
AC158186/c
LOCUS       AC158186               30844 bp    DNA     linear   PLN 26-MAY-2005
DEFINITION  Selaginella moellendorffii clone JGIASXY-5F17, complete sequence.
ACCESSION   AC158186
VERSION     AC158186.2  GI:66730719
KEYWORDS    HTG.
SOURCE      Selaginella moellendorffii
  ORGANISM  Selaginella moellendorffii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Lycopodiophyta; Isoetopsida; Selaginellales; Selaginellaceae;
            Selaginella.
REFERENCE   1  (bases 1 to 30844)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 30844)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAR-2005) Production Genomics Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive B100, Walnut Creek, CA
            94598-1698, USA
REFERENCE   3  (bases 1 to 30844)
  AUTHORS   Stanford Human Genome Center.
  CONSRTM   DOE Joint Genome Institute
  TITLE     Direct Submission
  JOURNAL   Submitted (26-MAY-2005) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On May 26, 2005 this sequence version replaced gi:60650325.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.9% of Sequence;
            Estimated Total Number of Errors is 0.
FEATURES             Location/Qualifiers
     source          1. .30844
                     /organism="Selaginella moellendorffii"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:88036"
                     /clone="JGIASXY-5F17"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 15;  Length 30844;
  Best Local Similarity   90.9%;  Pred. No. 1.5e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TTGGCAACAGTGGCATGCACCG 22
              ||||||  ||||||||||| |||
Db       2812 TTGGCACCAGTGGCATGCTCCG 2791
```

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RESULT 7
AL603830
LOCUS       AL603830              104771 bp    DNA     linear   ROD 09-FEB-2005
DEFINITION  Mouse DNA sequence from clone RP23-467E19 on chromosome 11 Contains
            the Map2k3 gene for mitogen activated protein kinase kinase 3, the
            Gtlf3a gene for gene trap locus F3a, the Gtlf3b gene for gene trap
            locus F3b and two CpG islands, complete sequence.
ACCESSION   AL603830
VERSION     AL603830.7  GI:17017794
KEYWORDS    HTG; CpG island; Gtlf3a; Gtlf3b; kinase; Map2K3.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 104771)
  AUTHORS   Clark,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-FEB-2005) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
            Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Nov 20, 2001 this sequence version replaced gi:16944205.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep ----------
            Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: vega@sanger.ac.uk
            ----------
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one subclone; and the assembly was confirmed by restriction digest,
            except on the rare occasion of the clone being a YAC.
            Sequence from the Mouse Genome Sequencing Consortium whole genome
            shotgun may have been used to confirm this sequence.  Sequence data
            from the whole genome shotgun alone has only been used where it has
            a phred quality of at least 30.
            RP23-467E19 is from the RPCI-23 Mouse BAC Library
            constructed by the group of Pieter de Jong.
            For further details see http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6.
FEATURES             Location/Qualifiers
     source          1. .104771
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="11"
                     /clone="RP23-467E19"
                     /clone_lib="RPCI-23"
     gene            complement(join(36672. .37719,38280. .38325,39423. .39562,
                     42295. .42372,42712. .42839,44702. .44818,45877. .45996,
                     46219. .46332,47130. .47178,47537. .47603,57212. .57429))
                     /gene="Map2k3"
                     /locus_tag="RP23-467E19.1-002"
     gene            complement(join(36672. .37719,38280. .38325,39423. .39562,
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                42295. .42372,42712. .42839,43921. .43972,44702. .44818,
                45877. .45996,46219. .46332,47130. .47178,47537. .47603,
                57212. .57429))
                /gene="Map2k3"
                /locus_tag="RP23-467E19.1-001"
     mRNA       complement(join(36672. .37719,38280. .38325,39423. .39562,
                42295. .42372,42712. .42839,44702. .44818,45877. .45996,
                46219. .46332,47130. .47178,47537. .47603,57212. .57429))
                /gene="Map2k3"
                /locus_tag="RP23-467E19.1-002"
                /product="mitogen activated protein kinase kinase 3"
                /note="match: cDNAs: BC007467.1"
     mRNA       complement(join(36672. .37719,38280. .38325,39423. .39562,
                42295. .42372,42712. .42839,43921. .43972,44702. .44818,
                45877. .45996,46219. .46332,47130. .47178,47537. .47603,
                57212. .57429))
                /gene="Map2k3"
                /locus_tag="RP23-467E19.1-002"
                /product="mitogen activated protein kinase kinase 3"
                /note="match: ESTs: AA008333.1 AA433619.1 AV238394.1
                AW106586.1 AW539252.1 BB858602.1 BF234702.1 BI555968.1
                BY019272.1 BY226967.1 BY685384.1 BY710384.1 CA569861.1
                CB947897.1 CB951524.1 W78467.1
                match: cDNAs: AK008141.1 AK011002.1 AK093838.1 BC032478.1
                D87116.1 U66839.1"
     CDS        complement(join(37636. .37719,38280. .38325,39423. .39562,
                42295. .42372,42712. .42839,43921. .43972,44702. .44818,
                45877. .45996,46219. .46332,47130. .47178,47537. .47603,
                57212. .57260))
                /gene="Map2k3"
                /locus_tag="RP23-467E19.1-002"
                /standard_name="OTTMUSP00000006687"
                /note="match: proteins: O09110 P46734"
                /codon_start=1
                /product="mitogen activated protein kinase kinase 3"
                /protein_id="CAI25794.1"
                /db_xref="GI:56237940"
                /db_xref="InterPro:IPR000719"
                /db_xref="InterPro:IPR002290"
                /db_xref="InterPro:IPR008271"
                /db_xref="InterPro:IPR011009"
                /translation="MESPAASPPASLPQTKGKSKRKKDLRISCVSKPPVSNPTPPRNL
                DSRTFITIGDRNFEVEADDLVTISELGRGAYGVVEKVRHAQSGTIMAVKRIRATVNTQ
                EQKRLLMDLDINMRTVDCFYTVTFYGALFREGDVWICMELMDTSLDKFYRKVLEKNMK
                IPEDILGEIAVSIVRALEHLHSKLSVIHRDVKPSNVLINKEGHVKMCDFGISGYLVDS
                VAKTMDAGCKPYMAPERINPELNQKGYNVKSDVWSLGITMIEMAILRFPYESWGTPFQ
                QLKQVVEEPSPQLPADQFSPEFVDFTSQCLRKNPAERMSYLELMEHPFFTLHKTKKTD
                IAAFVKEILGEDS"
     gene       complement(join(37662. .37719,38280. .38821))
                /gene="Map2k3"
                /locus_tag="RP23-467E19.1-006"
     mRNA       complement(join(37662. .37719,38280. .38821))
                /gene="Map2k3"
                /locus_tag="RP23-467E19.1-006"
                /product="mitogen activated protein kinase kinase 3"
                /note="match: ESTs: BF467851.1"
     gene       complement(join(41892. .42372,42712. .42839,43921. .43972,
                44702. .44818,45877. .45996,46219. .46332,47130. .47178,
                47537. .47603,57212. .57429))
                /gene="Map2k3"
                /locus_tag="RP23-467E19.1-003"
     mRNA       complement(join(41892. .42372,42712. .42839,43921. .43972,
                44702. .44818,45877. .45996,46219. .46332,47130. .47178,
                47537. .47603,57212. .57429))
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                     /gene="Map2k3"
                     /locus_tag="RP23-467E19.1-003"
                     /product="mitogen activated protein kinase kinase 3"
                     /note="match: ESTs: BB538636.2 BY724665.1
                     match: cDNAs: AK053378.1"
     gene            complement(join(42712. .42839,43921. .43972,44702. .44818,
                     45877. .45996,46219. .46332,47083. .47178,47537. .47603))
                     /gene="Map2k3"
                     /locus_tag="RP23-467E19.1-004"
     mRNA            complement(join(42712. .42839,43921. .43972,44702. .44818,
                     45877. .45996,46219. .46332,47083. .47178,47537. .47603))
                     /gene="Map2k3"
                     /locus_tag="RP23-467E19.1-004"
                     /product="mitogen activated protein kinase kinase 3"
                     /note="match: ESTs: BI525531.1"
     gene            complement(join(47367. .47603,57212. .57429))
                     /gene="Map2k3"
                     /locus_tag="RP23-467E19.1-005"
     mRNA            complement(join(47367. .47603,57212. .57429))
                     /gene="Map2k3"
                     /locus_tag="RP23-467E19.1-005"
                     /product="mitogen activated protein kinase kinase 3"
                     /note="match: ESTs: BB857429.1"
     gene            join(57616. .57917,67578. .68566)
                     /gene="Gtlf3a"
                     /locus_tag="RP23-467E19.2-001"
     mRNA            join(57616. .57917,67578. .68566)
                     /gene="Gtlf3a"
                     /locus_tag="RP23-467E19.2-001"
                     /product="gene trap locus F3a"
                     /note="match: ESTs: AI466976.1 AV085862.1 AV092279.1
                     AV253865.2 AV279917.1 BF099931.1 BY357260.1 BY709130.1
                     BY709606.1 BY709640.1
                     match: cDNAs: AK009371.1 AK010055.1 AK010107.1 BC031537.1"
     gene            join(74733. .74800,82483. .82601,83362. .83529)
                     /gene="Gtlf3b"
                     /locus_tag="RP23-467E19.3-002"
     mRNA            join(74733. .74800,82483. .82601,83362. .83529)
                     /gene="Gtlf3b"
                     /locus_tag="RP23-467E19.3-002"
                     /product="gene trap locus F3b"
                     /note="match: ESTs: BY176117.1 BY178036.1 BY190148.1"
     gene            join(75671. .75854,82483. .82601,83362. .87237)
                     /gene="Gtlf3b"
                     /locus_tag="RP23-467E19.3-001"
     mRNA            join(75671. .75854,82483. .82601,83362. .87237)
                     /gene="Gtlf3b"
                     /locus_tag="RP23-467E19.3-001"
                     /product="gene trap locus F3b"
                     /note="match: ESTs: AI413349.1 AI425923.1 BE308889.1
                     BE996115.1 BU152631.1 BY177308.1 BY196792.1 BY198579.1
                     BY202343.1 BY203840.1 BY747733.1
                     match: cDNAs: AK004720.2 AK080453.1 BC034332.1 BC038816.1"
     CDS             join(75758. .75854,82483. .82601,83362. .83478)
                     /gene="Gtlf3b"
                     /locus_tag="RP23-467E19.3-002"
                     /standard_name="OTTMUSP00000006007"
                     /note="match: proteins: Q8N6N6 Q9DBW3"
                     /codon_start=1
                     /product="gene trap locus F3b"
                     /protein_id="CAI25795.1"
                     /db_xref="GI:56237941"
                     /translation="MAHATPPSALEQGGPIRVEHDRQRRQFSVRLNGCHDRAVLLYEY
                     VGKRIVDLQHTEVPDAYRGRGIAKHLAKAALDFVVEEDLKAHLTCWYIQKYVKENPLP
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     polyA_signal    86401. .86406
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                     /locus_tag="RP23-467E19.3-001"
     polyA_site      86427
                     /gene="Gtlf3b"
                     /locus_tag="RP23-467E19.3-001"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 9;  Length 104771;
  Best Local Similarity   90.9%;  Pred. No. 1.4e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TTGGCAACAGTGGCATGCACCG 22
              |||||||||||| ||||||| |
Db       6473 TTGGCAACAGTGCCATGCACAG 6494


RESULT 8
AC161885
LOCUS       AC161885               206431 bp    DNA     linear   HTG 21-MAY-2005
DEFINITION  Gallus gallus chromosome UNKNOWN clone CH261-15B19, WORKING DRAFT
            SEQUENCE, 8 unordered pieces.
ACCESSION   AC161885
VERSION     AC161885.1  GI:66392501
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 206431)
  AUTHORS   Wilson,R.K.
  TITLE     The sequence of Gallus gallus clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 206431)
  AUTHORS   Wilson,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAY-2005) Genetics, Genome Sequencing Center, 4444
            Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT
            ----------------- Genome Center ----------------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu
            Contact: submissions@watson.wustl.edu
            -------------- Project Information -------------------
            Center project name: J_AA015B19
            ------------------------------------------------------
            -------------- Summary Statistics  --------------
            Sequencing vector: M13; 0%
            Sequencing vector: plasmid; 100%
            Chemistry: Dye-primer ET; 0% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 203515 bases at least Q40
            Consensus quality: 204721 bases at least Q30
            Consensus quality: 205241 bases at least Q20
            ------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 8 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
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            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     3949: contig of 3949 bp in length
            *     3950     4049: gap of unknown length
            *     4050     9460: contig of 5411 bp in length
            *     9461     9560: gap of unknown length
            *     9561    20832: contig of 11272 bp in length
            *    20833    20932: gap of unknown length
            *    20933    37073: contig of 16141 bp in length
            *    37074    37173: gap of unknown length
            *    37174    56455: contig of 19282 bp in length
            *    56456    56555: gap of unknown length
            *    56556   100723: contig of 44168 bp in length
            *   100724   100823: gap of unknown length
            *   100824   155191: contig of 54368 bp in length
            *   155192   155291: gap of unknown length
            *   155292   206431: contig of 51140 bp in length.
FEATURES             Location/Qualifiers
     source          1. .206431
                     /organism="Gallus gallus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9031"
                     /chromosome="UNKNOWN"
                     /clone="CH261-15B19"
     misc_feature    1. .3949
                     /note="assembly_name:Contig2
                     clone_end:T7
                     vector_side:right"
     gap             3950. .4049
                     /estimated_length=unknown
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                     /note="assembly_name:Contig3"
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     misc_feature    9561. .20832
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     gap             20833. .20932
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     misc_feature    20933. .37073
                     /note="assembly_name:Contig5"
     gap             37074. .37173
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     misc_feature    37174. .56455
                     /note="assembly_name:Contig6"
     gap             56456. .56555
                     /estimated_length=unknown
     misc_feature    56556. .100723
                     /note="assembly_name:Contig7"
     gap             100724. .100823
                     /estimated_length=unknown
     misc_feature    100824. .155191
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     gap             155192. .155291
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                     /note="assembly_name:Contig9"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 14;  Length 206431;
  Best Local Similarity   90.9%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TTGGCAACAGTGGCATGCACCG 22
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Db      26993 TTAGCAACAGTGGCATGCACAG 27014


RESULT 9
AC163712
LOCUS       AC163712               244279 bp    DNA     linear   HTG 13-JUN-2005
DEFINITION  Gallus gallus chromosome UNKNOWN clone CH261-29M9, WORKING DRAFT
            SEQUENCE, 32 unordered pieces.
ACCESSION   AC163712
VERSION     AC163712.1  GI:67515067
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 244279)
  AUTHORS   Wilson,R.K.
  TITLE     The sequence of Gallus gallus clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 244279)
  AUTHORS   Wilson,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUN-2005) Genetics, Genome Sequencing Center, 4444
            Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT
            ----------------- Genome Center ---------------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu
            Contact: submissions@watson.wustl.edu
            -------------- Project Information -------------------
            Center project name: J_AA029M09
            ------------------------------------------------------
            -------------- Summary Statistics  --------------
            Sequencing vector: M13; 0%
            Sequencing vector: plasmid; 100%
            Chemistry: Dye-primer ET; 0% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 231430 bases at least Q40
            Consensus quality: 235038 bases at least Q30
            Consensus quality: 237275 bases at least Q20
            ------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 32 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1283: contig of 1283 bp in length
            *     1284     1383: gap of unknown length
            *     1384     2584: contig of 1201 bp in length
            *     2585     2684: gap of unknown length
            *     2685     3930: contig of 1246 bp in length
            *     3931     4030: gap of unknown length
            *     4031     5280: contig of 1250 bp in length
            *     5281     5380: gap of unknown length
            *     5381     7337: contig of 1957 bp in length
            *     7338     7437: gap of unknown length
            *     7438     9021: contig of 1584 bp in length
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            *     9022     9121: gap of unknown length
            *     9122    11089: contig of 1968 bp in length
            *    11090    11189: gap of unknown length
            *    11190    13486: contig of 2297 bp in length
            *    13487    13586: gap of unknown length
            *    13587    15833: contig of 2247 bp in length
            *    15834    15933: gap of unknown length
            *    15934    17435: contig of 1502 bp in length
            *    17436    17535: gap of unknown length
            *    17536    19371: contig of 1836 bp in length
            *    19372    19471: gap of unknown length
            *    19472    22284: contig of 2813 bp in length
            *    22285    22384: gap of unknown length
            *    22385    25532: contig of 3148 bp in length
            *    25533    25632: gap of unknown length
            *    25633    30124: contig of 4492 bp in length
            *    30125    30224: gap of unknown length
            *    30225    33511: contig of 3287 bp in length
            *    33512    33611: gap of unknown length
            *    33612    36770: contig of 3159 bp in length
            *    36771    36870: gap of unknown length
            *    36871    42189: contig of 5319 bp in length
            *    42190    42289: gap of unknown length
            *    42290    46491: contig of 4202 bp in length
            *    46492    46591: gap of unknown length
            *    46592    50239: contig of 3648 bp in length
            *    50240    50339: gap of unknown length
            *    50340    54250: contig of 3911 bp in length
            *    54251    54350: gap of unknown length
            *    54351    58613: contig of 4263 bp in length
            *    58614    58713: gap of unknown length
            *    58714    67049: contig of 8336 bp in length
            *    67050    67149: gap of unknown length
            *    67150    74757: contig of 7608 bp in length
            *    74758    74857: gap of unknown length
            *    74858    82727: contig of 7870 bp in length
            *    82728    82827: gap of unknown length
            *    82828    93016: contig of 10189 bp in length
            *    93017    93116: gap of unknown length
            *    93117   105498: contig of 12382 bp in length
            *   105499   105598: gap of unknown length
            *   105599   119371: contig of 13773 bp in length
            *   119372   119471: gap of unknown length
            *   119472   132312: contig of 12841 bp in length
            *   132313   132412: gap of unknown length
            *   132413   154469: contig of 22057 bp in length
            *   154470   154569: gap of unknown length
            *   154570   175487: contig of 20918 bp in length
            *   175488   175587: gap of unknown length
            *   175588   197601: contig of 22014 bp in length
            *   197602   197701: gap of unknown length
            *   197702   244279: contig of 46578 bp in length.
FEATURES             Location/Qualifiers
     source          1. .244279
                     /organism="Gallus gallus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9031"
                     /chromosome="UNKNOWN"
                     /clone="CH261-29M9"
     misc_feature    1. .1283
                     /note="assembly_name:Contig16"
     gap             1284. .1383
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     misc_feature    1384. .2584
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misc_feature    15934. .17435
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gap             17436. .17535
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misc_feature    17536. .19371
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gap             19372. .19471
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                /note="assembly_name:Contig41"
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  Query Match             85.5%;  Score 18.8;  DB 14;  Length 244279;
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  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TTGGCAACAGTGGCATGCACCG 22
              || |||||||||||||||| |
Db     170397 TTAGCAACAGTGGCATGCACAG 170418


RESULT 10
AC098544
LOCUS       AC098544               248883 bp    DNA     linear   HTG 10-MAY-2003
DEFINITION  Rattus norvegicus clone CH230-103A8, *** SEQUENCING IN PROGRESS
            ***, 5 unordered pieces.
ACCESSION   AC098544
VERSION     AC098544.6  GI:30521653
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 248883)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
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            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
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            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
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            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
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            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
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            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
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Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 248883)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (24-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 248883)

AUTHORS Rat Genome Sequencing Consortium.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On May 10, 2003 this sequence version replaced gi:22855582.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
---------- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
---------- Project Information
Center project name: GHJG
Center clone name: CH230-103A8
---------- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 223541 bases at least Q40
Consensus quality: 226408 bases at least Q30
Consensus quality: 228553 bases at least Q20
Estimated insert size: 235340; sum-of-contigs estimation

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            Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 5 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1   242485: contig of 242485 bp in length
            *   242486   242585: gap of unknown length
            *   242586   243738: contig of 1153 bp in length
            *   243739   243838: gap of unknown length
            *   243839   245069: contig of 1231 bp in length
            *   245070   245169: gap of unknown length
            *   245170   246652: contig of 1483 bp in length
            *   246653   246752: gap of unknown length
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FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 14;  Length 248883;
  Best Local Similarity   90.9%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TTGGCAACAGTGGCATGCACCG 22
              |||||||||||| ||||||| |
Db      70892 TTGGCAACAGTGCCATGCACAG 70913


RESULT 11
AC118088
LOCUS       AC118088              259215 bp    DNA     linear   HTG 19-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-30B23, WORKING DRAFT SEQUENCE.
ACCESSION   AC118088
VERSION     AC118088.5  GI:25087858
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 259215)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
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Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 259215)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (13-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 259215)

AUTHORS Rat Genome Sequencing Consortium.

TITLE Direct Submission

JOURNAL Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On Nov 19, 2002 this sequence version replaced gi:23265586.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described

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            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            ---------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            ---------- Project Information
                Center project name: GUPO
                Center clone name: CH230-30B23
            ---------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 238249 bases at least Q40
                Consensus quality: 240765 bases at least Q30
                Consensus quality: 242460 bases at least Q20
                Estimated insert size: 245419; sum-of-contigs estimation
                Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
            ----------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 1 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *        1   259215: contig of 259215 bp in length.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-30B23"
     misc_feature    1. .1448
                     /note="wgs_end_extension
                     clone_end:Sp6"
     misc_feature    1577. .3317
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                     clone_end:Sp6"
     misc_feature    3368. .4702
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     misc_feature    complement(255901. .256586)
                     /note="clone_boundary
                     clone_end:T7
                     site:
                     end_sequence:BH290550"
ORIGIN
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Query Match 85.5%; Score 18.8; DB 14; Length 259215;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 TTGGCAACAGTGGCATGCACCG 22
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Db      97487 TTGGCAACAGTGCCATGCACAG 97508
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RESULT 12
AC120483
LOCUS AC120483 262976 bp DNA linear HTG 15-NOV-2002
DEFINITION Rattus norvegicus clone CH230-13K13, WORKING DRAFT SEQUENCE, 2 unordered pieces.
ACCESSION AC120483
VERSION AC120483.4 GI:25008120
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 262976)
AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,

Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 262976)

AUTHORS Worley,K.C.

TITLE Direct Submission

JOURNAL Submitted (07-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 262976)

AUTHORS Rat Genome Sequencing Consortium.

TITLE Direct Submission

JOURNAL Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On Nov 15, 2002 this sequence version replaced gi:23265426.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
---------- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
---------- Project Information
Center project name: GXNG
Center clone name: CH230-13K13
---------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 242345 bases at least Q40
Consensus quality: 245593 bases at least Q30
Consensus quality: 247807 bases at least Q20
Estimated insert size: 249832; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 258816: contig of 258816 bp in length
* 258817 258916: gap of unknown length
* 258917 262976: contig of 4060 bp in length.

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                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-13K13"
     misc_feature    1. .1927
                     /note="wgs_end_extension
                     clone_end:Sp6"
     misc_feature    complement(5096. .5877)
                     /note="clone_boundary
                     clone_end:Sp6
                     site:
                     end_sequence:BH274933"
     misc_feature    137741. .139060
                     /note="wgs_contig"
     misc_feature    complement(256373. .257121)
                     /note="clone_boundary
                     clone_end:T7
                     site:
                     end_sequence:BH274931"
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                     clone_end:T7"
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  Best Local Similarity   90.9%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TTGGCAACAGTGGCATGCACCG 22
              |||||||||||| ||||||| |
Db      45102 TTGGCAACAGTGCCATGCACAG 45123


RESULT 13
AC096627/c
LOCUS       AC096627               264908 bp    DNA     linear   ROD 03-MAY-2003
DEFINITION  Mus musculus strain C57BL/6J clone rp23-77b23 map 11, complete
            sequence.
ACCESSION   AC096627
VERSION     AC096627.28  GI:30349025
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 264908)
  AUTHORS   Ni,Y., Song,L. and Roe,B.A.
  TITLE     Mus musculus BAC Clone rp23-77b23
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 264908)
  AUTHORS   Ni,Y., Song,L. and Roe,B.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-SEP-2001) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE   3  (bases 1 to 264908)
  AUTHORS   Ni,Y., Song,L. and Roe,B.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-MAY-2003) Department Of Chemistry And Biochemistry,
```

```
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
REFERENCE   4  (bases 1 to 264908)
  AUTHORS   Ni,Y., Song,L. and Roe,B.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-MAY-2003) Department Of Chemistry And Biochemistry,
            The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
            OK 73019, USA
COMMENT     On May 3, 2003 this sequence version replaced gi:29423919.
            -------------- Genome Center
            Center: Department Of Chemistry And Biochemistry
            The University Of Oklahoma
            Center code:UOKNOR
            ----------------------.
FEATURES             Location/Qualifiers
     source          1. .264908
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /map="11"
                     /clone="rp23-77b23"
                     /clone_lib="RPCI - 23 Female (C57BL/6J) Mouse BAC Library"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 9;  Length 264908;
  Best Local Similarity   90.9%;  Pred. No. 1.3e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TTGGCAACAGTGGCATGCACCG 22
              |||||||||||| ||||||| |
Db     172994 TTGGCAACAGTGCCATGCACAG 172973


RESULT 14
BA000023_21
WPCOMMENT
  Sequence split into 27 fragments  LOCUS BA000023 Accession BA000023
     Fragment Name      Begin     End
     BA000023_00            1    110000
     BA000023_01       100001    210000
     BA000023_02       200001    310000
     BA000023_03       300001    410000
     BA000023_04       400001    510000
     BA000023_05       500001    610000
     BA000023_06       600001    710000
     BA000023_07       700001    810000
     BA000023_08       800001    910000
     BA000023_09       900001   1010000
     BA000023_10      1000001   1110000
     BA000023_11      1100001   1210000
     BA000023_12      1200001   1310000
     BA000023_13      1300001   1410000
     BA000023_14      1400001   1510000
     BA000023_15      1500001   1610000
     BA000023_16      1600001   1710000
     BA000023_17      1700001   1810000
     BA000023_18      1800001   1910000
     BA000023_19      1900001   2010000
     BA000023_20      2000001   2110000
     BA000023_21      2100001   2210000
     BA000023_22      2200001   2310000
     BA000023_23      2300001   2410000
     BA000023_24      2400001   2510000
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     BA000023_25       2500001   2610000
     BA000023_26       2600001   2694756
Continuation (22 of 27) of BA000023 from base 2100001 (BA000023 Sulfolobus tokodaii str. 7 DN

  Query Match             83.6%;  Score 18.4;  DB 1;  Length 110000;
  Best Local Similarity   95.0%;  Pred. No. 2.2e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TGGCAACAGTGGCATGCACC 21
              |||||||||||| |||||||
Db     100593 TGGCAACAGTGGAATGCACC 100612


RESULT 15
BA000023_22
WPCOMMENT
  Sequence split into 27 fragments  LOCUS BA000023 Accession BA000023
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     BA000023_01       100001    210000
     BA000023_02       200001    310000
     BA000023_03       300001    410000
     BA000023_04       400001    510000
     BA000023_05       500001    610000
     BA000023_06       600001    710000
     BA000023_07       700001    810000
     BA000023_08       800001    910000
     BA000023_09       900001   1010000
     BA000023_10      1000001   1110000
     BA000023_11      1100001   1210000
     BA000023_12      1200001   1310000
     BA000023_13      1300001   1410000
     BA000023_14      1400001   1510000
     BA000023_15      1500001   1610000
     BA000023_16      1600001   1710000
     BA000023_17      1700001   1810000
     BA000023_18      1800001   1910000
     BA000023_19      1900001   2010000
     BA000023_20      2000001   2110000
     BA000023_21      2100001   2210000
     BA000023_22      2200001   2310000
     BA000023_23      2300001   2410000
     BA000023_24      2400001   2510000
     BA000023_25      2500001   2610000
     BA000023_26      2600001   2694756
Continuation (23 of 27) of BA000023 from base 2200001 (BA000023 Sulfolobus tokodaii str. 7 DN

  Query Match             83.6%;  Score 18.4;  DB 1;  Length 110000;
  Best Local Similarity   95.0%;  Pred. No. 2.2e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 TGGCAACAGTGGCATGCACC 21
              |||||||||||| |||||||
Db        593 TGGCAACAGTGGAATGCACC 612


Search completed: May  7, 2006, 07:20:01
Job time : 518.074 secs
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